

O'Bryen, Barbara

From: Switzer, Juliet
Sent: Wednesday, January 05, 2005 1:19 PM
To: O'Bryen, Barbara
Subject: please search

08-956991 in US PATS- issued and pending

1. Seq id no 1
2. Seq id no 10
3. nucleotides 453-6185 of seq id no 1
4. nucleotides 453-5168 of seq id no 10
5. oligomer of at least 50 nucleotides from seq id no 1 or seq id no 10.

please return results on disk.

THANK YOU.

Juliet Switzer
Art Unit 1634
phone: 571-272-753
office: Remsen 2D75

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OM nucleic - nucleic search, using sw model

Run on: January 6, 2005, 19:14:13 ; Search time 232.323 Seconds
(without alignments)
14428.522 Million cell updates/sec

Title: US-08-956-991-10_COPY_453_5168
Perfect score: 4716
Sequence: 1 atgtggatactggctctctc.....gatgcaaagagtttagctga 4716

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1806.8	38.3	5824	4	US-09-620-312D-72	Sequence 72, Appl
2	529.2	11.2	1493	2	US-08-752-307B-6	Sequence 6, Appli
3	529.2	11.2	1493	3	US-09-707-802-6	Sequence 6, Appli
4	529.2	11.2	1493	3	US-09-991-326-6	Sequence 6, Appli
5	133.4	2.8	757	4	US-09-270-767-12893	Sequence 12893, A
6	66.4	1.4	4078	4	US-09-016-434-1132	Sequence 1132, Ap
7	66.4	1.4	6000	1	US-08-348-006B-6	Sequence 6, Appli
8	66.4	1.4	6000	2	US-08-800-825A-6	Sequence 6, Appli
9	66.4	1.4	6000	3	US-09-158-657-6	Sequence 6, Appli
10	66.4	1.4	6000	5	PCT-US94-10166-6	Sequence 6, Appli
11	66.2	1.4	2401	3	US-09-724-864-1	Sequence 1, Appli

	12	63.2	1.3	6363	4	US-09-023-655-879	Sequence 879, App
	13	57	1.2	7702	4	US-09-023-655-1336	Sequence 1336, Ap
	14	57	1.2	7702	4	US-09-743-492A-3	Sequence 3, Appli
c	15	56.2	1.2	367	4	US-09-270-767-394	Sequence 394, App
c	16	56.2	1.2	367	4	US-09-270-767-15676	Sequence 15676, A
	17	53.8	1.1	7108	4	US-09-822-871-1	Sequence 1, Appli
	18	47.8	1.0	2600	2	US-08-427-497E-4	Sequence 4, Appli
	19	47.8	1.0	3189	2	US-08-427-497E-3	Sequence 3, Appli
	20	47.8	1.0	3774	2	US-08-341-843B-1	Sequence 1, Appli
	21	47.8	1.0	3774	2	US-08-427-497E-1	Sequence 1, Appli
	22	47.8	1.0	3774	2	US-08-427-497E-2	Sequence 2, Appli
	23	47.8	1.0	3888	3	US-08-506-296B-13	Sequence 13, Appl
	24	45.8	1.0	5690	2	US-08-447-464-2	Sequence 2, Appli
	25	45.8	1.0	5690	2	US-08-716-679-2	Sequence 2, Appli
	26	45.2	1.0	4608	3	US-09-041-886-24	Sequence 24, Appl
	27	45.2	1.0	4608	5	PCT-US94-05277-1	Sequence 1, Appli
	28	45.2	1.0	7647	4	US-09-566-921-75	Sequence 75, Appl
	29	44.6	0.9	4843	3	US-08-986-485-1	Sequence 1, Appli
	30	44.2	0.9	4080	4	US-09-016-434-1326	Sequence 1326, Ap
	31	44.2	0.9	5506	4	US-09-976-594-530	Sequence 530, App
	32	44.2	0.9	5645	4	US-09-023-655-1319	Sequence 1319, Ap
	33	44.2	0.9	5681	4	US-09-919-172-58	Sequence 58, Appl
	34	44.2	0.9	5933	4	US-09-919-172-23	Sequence 23, Appl
	35	42.8	0.9	4975	2	US-08-249-687C-1	Sequence 1, Appli
	36	42.8	0.9	4989	2	US-08-666-392A-3	Sequence 3, Appli
	37	42.8	0.9	4989	2	US-08-625-819-1	Sequence 1, Appli
	38	42.8	0.9	4989	3	US-08-755-558-4	Sequence 4, Appli
	39	42.8	0.9	4989	3	US-08-746-559A-1	Sequence 1, Appli
	40	42.8	0.9	4989	3	US-08-880-313A-9	Sequence 9, Appli
	41	42.8	0.9	4989	3	US-09-199-926-3	Sequence 3, Appli
	42	42.8	0.9	4989	3	US-09-389-855A-9	Sequence 9, Appli
	43	42.8	0.9	4989	3	US-09-668-822-9	Sequence 9, Appli
	44	42.8	0.9	4989	4	US-09-343-551-1	Sequence 1, Appli
	45	42.8	0.9	4989	4	US-09-023-655-1306	Sequence 1306, Ap

OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 22:32:49 ; Search time 330.276 Seconds
(without alignments)
14212.502 Million cell updates/sec

Title: US-08-956-991-1
Perfect score: 6604
Sequence: 1 tgactgaggccggagcacgg.....gaaaattgccaaaatatatt 6604

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size : 50

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query
No.	Score	Match Length DB ID Description

No matches found

Search completed: January 8, 2005, 16:40:14
Job time : 330.276 secs

OM nucleic - nucleic search, using sw model

Run on: January 8, 2005, 00:29:35 ; Search time 15074 Seconds
(without alignments)
17765.558 Million cell updates/sec

Title: US-08-956-991-1
Perfect score: 6604
Sequence: 1 tgactgaggccggagcacgg.....gaaaattgccaaaatatatt 6604

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 44308572 seqs, 20275418765 residues

Word size : 50

Total number of hits satisfying chosen parameters: 136

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Pending_Patents_NA_Main:*

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OM nucleic - nucleic search, using sw model

Run on: January 8, 2005, 00:48:35 ; Search time 724.984 Seconds
(without alignments)
15321.252 Million cell updates/sec

Title: US-08-956-991-1
Perfect score: 6604
Sequence: 1 tgactgaggccggagcacgg.....gaaaattgccaaaatatatt 6604

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1829893 seqs, 840979846 residues

Word size : 50

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Pending Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq1:*
8: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:*
9: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query
No.	Score	Match Length DB ID Description

No matches found

Search completed: January 9, 2005, 01:19:35
Job time : 724.984 secs

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OM nucleic - nucleic search, using sw model

Run on: January 8, 2005, 00:48:35 ; Search time 724.984 Seconds
(without alignments)
15321.252 Million cell updates/sec

Title: US-08-956-991-1
Perfect score: 6604
Sequence: 1 tgactgaggccggagcacgg.....gaaaattgccaaaatatatt 6604

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1829893 seqs, 840979846 residues

Word size : 50

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Pending Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq1:*
8: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:*
9: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query
No.	Score	Match Length DB ID Description

No matches found

Search completed: January 9, 2005, 01:19:35
Job time : 724.984 secs

OM nucleic - nucleic search, using sw model

Run on: January 8, 2005, 00:48:35 ; Search time 704.016 Seconds
(without alignments)
15321.252 Million cell updates/sec

Title: US-08-956-991-10
Perfect score: 6413
Sequence: 1 tgactgaggccggagcacgg.....gaaaattgccaaaatatatt 6413

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1829893 seqs, 840979846 residues

Word size : 50

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq1:*
8: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:*
9: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

%
Result Query
No. Score Match Length DB ID Description

No matches found

Search completed: January 9, 2005, 01:19:35
Job time : 704.016 secs

OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 22:32:49 ; Search time 320.724 Seconds
(without alignments)
14212.502 Million cell updates/sec

Title: US-08-956-991-10
Perfect score: 6413
Sequence: 1 tgactgaggccggagcacgg.....gaaaattgccaaaatatatt 6413

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size : 50

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query
No.	Score	Match Length DB ID Description

No matches found

Search completed: January 8, 2005, 16:40:14
Job time : 320.724 secs

OM nucleic - nucleic search, using sw model

Run on: January 8, 2005, 00:29:35 ; Search time 14638 Seconds
(without alignments)
17765.558 Million cell updates/sec

Title: US-08-956-991-10
Perfect score: 6413
Sequence: 1 tgactgaggccggagcacgg.....gaaaattgccaaaatatatt 6413

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 44308572 seqs, 20275418765 residues

Word size : 50

Total number of hits satisfying chosen parameters: 134

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Pending_Patents_NA_Main:*

- 1: /cgn2_6/ptodata/1/pna/PCTUS1_COMB.seq:*
- 2: /cgn2_6/ptodata/1/pna/PCTUS2_COMB.seq:*
- 3: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
- 4: /cgn2_6/ptodata/1/pna/US07_COMB.seq:*
- 5: /cgn2_6/ptodata/1/pna/US080_COMB.seq:*
- 6: /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
- 7: /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
- 8: /cgn2_6/ptodata/1/pna/US083_COMB.seq:*
- 9: /cgn2_6/ptodata/1/pna/US084_COMB.seq:*
- 10: /cgn2_6/ptodata/1/pna/US085_COMB.seq:*
- 11: /cgn2_6/ptodata/1/pna/US086_COMB.seq:*
- 12: /cgn2_6/ptodata/1/pna/US087_COMB.seq:*
- 13: /cgn2_6/ptodata/1/pna/US088_COMB.seq:*
- 14: /cgn2_6/ptodata/1/pna/US089_COMB.seq:*
- 15: /cgn2_6/ptodata/1/pna/US090_COMB.seq:*
- 16: /cgn2_6/ptodata/1/pna/US091_COMB.seq:*
- 17: /cgn2_6/ptodata/1/pna/US092A_COMB.seq:*
- 18: /cgn2_6/ptodata/1/pna/US092B_COMB.seq:*
- 19: /cgn2_6/ptodata/1/pna/US093A_COMB.seq:*
- 20: /cgn2_6/ptodata/1/pna/US093B_COMB.seq:*
- 21: /cgn2_6/ptodata/1/pna/US094_COMB.seq:*
- 22: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:*
- 23: /cgn2_6/ptodata/1/pna/US095B_COMB.seq:*
- 24: /cgn2_6/ptodata/1/pna/US095C_COMB.seq:*
- 25: /cgn2_6/ptodata/1/pna/US095D_COMB.seq:*
- 26: /cgn2_6/ptodata/1/pna/US096A_COMB.seq:*
- 27: /cgn2_6/ptodata/1/pna/US096B_COMB.seq:*
- 28: /cgn2_6/ptodata/1/pna/US096C_COMB.seq:*
- 29: /cgn2_6/ptodata/1/pna/US096D_COMB.seq:*
- 30: /cgn2_6/ptodata/1/pna/US096E_COMB.seq:*
- 31: /cgn2_6/ptodata/1/pna/US097A_COMB.seq:*
- 32: /cgn2_6/ptodata/1/pna/US097B_COMB.seq:*

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OM nucleic - nucleic search, using sw model

Run on: January 6, 2005, 19:14:13 ; Search time 315.922 Seconds
(without alignments)
14428.522 Million cell updates/sec

Title: US-08-956-991-10
Perfect score: 6413
Sequence: 1 tgactgaggccggagcacgg.....gaaaattgccaaaatatatt 6413

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%		Query			Description
Result	No.	Score	Match	Length	DB	ID	
	1	1922	30.0	5824	4	US-09-620-312D-72	Sequence 72, Appl
	2	541	8.4	1493	2	US-08-752-307B-6	Sequence 6, Appli
	3	541	8.4	1493	3	US-09-707-802-6	Sequence 6, Appli
	4	541	8.4	1493	3	US-09-991-326-6	Sequence 6, Appli
	5	133.4	2.1	757	4	US-09-270-767-12893	Sequence 12893, A
c	6	79.6	1.2	2561	4	US-09-616-289-48	Sequence 48, Appl
c	7	78.2	1.2	1614	4	US-09-616-289-45	Sequence 45, Appl
c	8	78.2	1.2	12425	4	US-09-616-289-50	Sequence 50, Appl
	9	73.4	1.1	320	3	US-09-165-264-7	Sequence 7, Appli
c	10	73.4	1.1	152331	3	US-09-128-155-16	Sequence 16, Appl
	11	72.4	1.1	320	3	US-09-165-264-13	Sequence 13, Appl

c	12	70.8	1.1	114793	4	US-10-148-806-3	Sequence 3, Appli
	13	69.8	1.1	320	3	US-09-165-264-14	Sequence 14, Appl
	14	69	1.1	318	3	US-09-165-264-12	Sequence 12, Appl
	15	69	1.1	319	3	US-09-165-264-8	Sequence 8, Appli
	16	69	1.1	320	3	US-09-165-264-11	Sequence 11, Appl
	17	66.4	1.0	4078	4	US-09-016-434-1132	Sequence 1132, Ap
	18	66.4	1.0	6000	1	US-08-348-006B-6	Sequence 6, Appli
	19	66.4	1.0	6000	2	US-08-800-825A-6	Sequence 6, Appli
	20	66.4	1.0	6000	3	US-09-158-657-6	Sequence 6, Appli
	21	66.4	1.0	6000	5	PCT-US94-10166-6	Sequence 6, Appli
	22	66.2	1.0	2401	3	US-09-724-864-1	Sequence 1, Appli
c	23	66	1.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	24	66	1.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	25	65.2	1.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	26	63.4	1.0	1203	3	US-09-086-010-1	Sequence 1, Appli
	27	63.2	1.0	6363	4	US-09-023-655-879	Sequence 879, App
	28	63	1.0	3507	2	US-08-775-009-36	Sequence 36, Appl
	29	62.6	1.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	30	62.2	1.0	801	2	US-08-770-379-16	Sequence 16, Appl
c	31	62.2	1.0	801	3	US-08-757-669A-16	Sequence 16, Appl
c	32	62.2	1.0	801	3	US-09-230-371A-16	Sequence 16, Appl
	33	62	1.0	4257	2	US-08-690-473-1	Sequence 1, Appli
	34	62	1.0	4257	3	US-09-259-821A-1	Sequence 1, Appli
	35	62	1.0	4257	3	US-08-843-659-1	Sequence 1, Appli
	36	62	1.0	4257	4	US-09-825-288A-1	Sequence 1, Appli
c	37	62	1.0	12001	1	US-08-458-568A-11	Sequence 11, Appl
c	38	61.6	1.0	4403	2	US-08-284-941-1	Sequence 1, Appli
c	39	61.6	1.0	4403	2	US-08-447-642-1	Sequence 1, Appli
c	40	61.6	1.0	4403	3	US-09-236-503-1	Sequence 1, Appli
c	41	61.6	1.0	4403	5	PCT-US93-02147A-1	Sequence 1, Appli
c	42	61.2	1.0	8147	3	US-09-514-247A-9	Sequence 9, Appli
c	43	60.6	0.9	801	3	US-09-298-568-3	Sequence 3, Appli
c	44	60.6	0.9	801	4	US-09-894-273-3	Sequence 3, Appli
	45	60.4	0.9	8438	1	US-07-945-283-1	Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: January 6, 2005, 19:14:13 ; Search time 282.423 Seconds
(without alignments)
14428.522 Million cell updates/sec

Title: US-08-956-991-1_COPY_453_6185
Perfect score: 5733
Sequence: 1 atgtggatactggctctctc.....tagaatggactttttgttaa 5733

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query				Description
	No.	Score	Match	Length	DB	ID			
1	2127.4	37.1	5824	4	US-09-620-312D-72	Sequence 72, Appl			
2	529.2	9.2	1493	2	US-08-752-307B-6	Sequence 6, Appli			
3	529.2	9.2	1493	3	US-09-707-802-6	Sequence 6, Appli			
4	529.2	9.2	1493	3	US-09-991-326-6	Sequence 6, Appli			
5	133.4	2.3	757	4	US-09-270-767-12893	Sequence 12893, A			
6	66.4	1.2	4078	4	US-09-016-434-1132	Sequence 1132, Ap			
7	66.4	1.2	6000	1	US-08-348-006B-6	Sequence 6, Appli			
8	66.4	1.2	6000	2	US-08-800-825A-6	Sequence 6, Appli			
9	66.4	1.2	6000	3	US-09-158-657-6	Sequence 6, Appli			
10	66.4	1.2	6000	5	PCT-US94-10166-6	Sequence 6, Appli			
11	66.2	1.2	2401	3	US-09-724-864-1	Sequence 1, Appli			

	12	63.2	1.1	6363	4	US-09-023-655-879	Sequence 879, App
	13	57	1.0	7702	4	US-09-023-655-1336	Sequence 1336, Ap
	14	57	1.0	7702	4	US-09-743-492A-3	Sequence 3, Appli
c	15	56.2	1.0	367	4	US-09-270-767-394	Sequence 394, App
c	16	56.2	1.0	367	4	US-09-270-767-15676	Sequence 15676, A
	17	53.8	0.9	7108	4	US-09-822-871-1	Sequence 1, Appli
	18	47.8	0.8	2600	2	US-08-427-497E-4	Sequence 4, Appli
	19	47.8	0.8	3189	2	US-08-427-497E-3	Sequence 3, Appli
	20	47.8	0.8	3774	2	US-08-341-843B-1	Sequence 1, Appli
	21	47.8	0.8	3774	2	US-08-427-497E-1	Sequence 1, Appli
	22	47.8	0.8	3774	2	US-08-427-497E-2	Sequence 2, Appli
	23	47.8	0.8	3888	3	US-08-506-296B-13	Sequence 13, Appl
	24	45.8	0.8	5690	2	US-08-447-464-2	Sequence 2, Appli
	25	45.8	0.8	5690	2	US-08-716-679-2	Sequence 2, Appli
	26	45.2	0.8	4608	3	US-09-041-886-24	Sequence 24, Appl
	27	45.2	0.8	4608	5	PCT-US94-05277-1	Sequence 1, Appli
	28	45.2	0.8	7647	4	US-09-566-921-75	Sequence 75, Appl
	29	44.6	0.8	4843	3	US-08-986-485-1	Sequence 1, Appli
	30	44.2	0.8	4080	4	US-09-016-434-1326	Sequence 1326, Ap
	31	44.2	0.8	5506	4	US-09-976-594-530	Sequence 530, App
	32	44.2	0.8	5645	4	US-09-023-655-1319	Sequence 1319, Ap
	33	44.2	0.8	5681	4	US-09-919-172-58	Sequence 58, Appl
	34	44.2	0.8	5933	4	US-09-919-172-23	Sequence 23, Appl
	35	43.8	0.8	461	4	US-09-270-767-814	Sequence 814, App
	36	43.8	0.8	461	4	US-09-270-767-16096	Sequence 16096, A
	37	42.8	0.7	4975	2	US-08-249-687C-1	Sequence 1, Appli
	38	42.8	0.7	4989	2	US-08-666-392A-3	Sequence 3, Appli
	39	42.8	0.7	4989	2	US-08-625-819-1	Sequence 1, Appli
	40	42.8	0.7	4989	3	US-08-755-558-4	Sequence 4, Appli
	41	42.8	0.7	4989	3	US-08-746-559A-1	Sequence 1, Appli
	42	42.8	0.7	4989	3	US-08-880-313A-9	Sequence 9, Appli
	43	42.8	0.7	4989	3	US-09-199-926-3	Sequence 3, Appli
	44	42.8	0.7	4989	3	US-09-389-855A-9	Sequence 9, Appli
	45	42.8	0.7	4989	3	US-09-668-822-9	Sequence 9, Appli

OM nucleic - nucleic search, using sw model

Run on: January 6, 2005, 19:14:13 ; Search time 325.331 Seconds
 (without alignments)
 14428.522 Million cell updates/sec

Title: US-08-956-991-1
 Perfect score: 6604
 Sequence: 1 tgactgaggccggagcacgg.....gaaaattgccaaaatatatt 6604

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:*
 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query				Description
	No.	Score	Match	Length	DB	ID			
	1	2127.4	32.2	5824	4	US-09-620-312D-72			Sequence 72, Appl
	2	541	8.2	1493	2	US-08-752-307B-6			Sequence 6, Appli
	3	541	8.2	1493	3	US-09-707-802-6			Sequence 6, Appli
	4	541	8.2	1493	3	US-09-991-326-6			Sequence 6, Appli
	5	133.4	2.0	757	4	US-09-270-767-12893			Sequence 12893, A
c	6	79.6	1.2	2561	4	US-09-616-289-48			Sequence 48, Appl
c	7	78.2	1.2	1614	4	US-09-616-289-45			Sequence 45, Appl
c	8	78.2	1.2	12425	4	US-09-616-289-50			Sequence 50, Appl
	9	73.4	1.1	320	3	US-09-165-264-7			Sequence 7, Appli
c	10	73.4	1.1	152331	3	US-09-128-155-16			Sequence 16, Appl
	11	72.4	1.1	320	3	US-09-165-264-13			Sequence 13, Appl
c	12	70.8	1.1	114793	4	US-10-148-806-3			Sequence 3, Appli

	13	69.8	1.1	320	3	US-09-165-264-14	Sequence 14, Appl
	14	69	1.0	318	3	US-09-165-264-12	Sequence 12, Appl
	15	69	1.0	319	3	US-09-165-264-8	Sequence 8, Appli
	16	69	1.0	320	3	US-09-165-264-11	Sequence 11, Appl
	17	66.4	1.0	4078	4	US-09-016-434-1132	Sequence 1132, Ap
	18	66.4	1.0	6000	1	US-08-348-006B-6	Sequence 6, Appli
	19	66.4	1.0	6000	2	US-08-800-825A-6	Sequence 6, Appli
	20	66.4	1.0	6000	3	US-09-158-657-6	Sequence 6, Appli
	21	66.4	1.0	6000	5	PCT-US94-10166-6	Sequence 6, Appli
	22	66.2	1.0	2401	3	US-09-724-864-1	Sequence 1, Appli
c	23	66	1.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	24	66	1.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	25	65.2	1.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	26	63.4	1.0	1203	3	US-09-086-010-1	Sequence 1, Appli
	27	63.2	1.0	6363	4	US-09-023-655-879	Sequence 879, App
	28	63	1.0	3507	2	US-08-775-009-36	Sequence 36, Appl
	29	62.6	0.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	30	62.2	0.9	801	2	US-08-770-379-16	Sequence 16, Appl
c	31	62.2	0.9	801	3	US-08-757-669A-16	Sequence 16, Appl
c	32	62.2	0.9	801	3	US-09-230-371A-16	Sequence 16, Appl
	33	62	0.9	4257	2	US-08-690-473-1	Sequence 1, Appli
	34	62	0.9	4257	3	US-09-259-821A-1	Sequence 1, Appli
	35	62	0.9	4257	3	US-08-843-659-1	Sequence 1, Appli
	36	62	0.9	4257	4	US-09-825-288A-1	Sequence 1, Appli
c	37	62	0.9	12001	1	US-08-458-568A-11	Sequence 11, Appl
c	38	61.6	0.9	4403	2	US-08-284-941-1	Sequence 1, Appli
c	39	61.6	0.9	4403	2	US-08-447-642-1	Sequence 1, Appli
c	40	61.6	0.9	4403	3	US-09-236-503-1	Sequence 1, Appli
c	41	61.6	0.9	4403	5	PCT-US93-02147A-1	Sequence 1, Appli
c	42	61.2	0.9	8147	3	US-09-514-247A-9	Sequence 9, Appli
c	43	60.6	0.9	801	3	US-09-298-568-3	Sequence 3, Appli
c	44	60.6	0.9	801	4	US-09-894-273-3	Sequence 3, Appli
	45	60.4	0.9	8438	1	US-07-945-283-1	Sequence 1, Appli